

#12



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SEP 11 2002

TIME: 10:17 ~~20~~

TECH CENTER 1600/2900

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Output Set: N:\CRF3\09052002\I881050.raw

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3 <110> APPLICANT: CROZE, EDWARD M.
4   FAULDS, DARYL
5   WAGNER, T. CHARIS
7 <120> TITLE OF INVENTION: NOVEL INTERFERON FOR THE TREATMENT OF MULTIPLE
8   SCLEROSIS
10 <130> FILE REFERENCE: BERLX-88
12 <140> CURRENT APPLICATION NUMBER: 09/881,050
13 <141> CURRENT FILING DATE: 2001-06-15
15 <150> PRIOR APPLICATION NUMBER: 60/212,046
16 <151> PRIOR FILING DATE: 2000-06-16
18 <160> NUMBER OF SEQ ID NOS: 30
20 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 24
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
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62 <211> LENGTH: 33
63 <212> TYPE: DNA
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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/881,050

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81     oligonucleotide
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92 <220> FEATURE:
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106 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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111 1 5
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117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
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125 1 5
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129 <211> LENGTH: 5
130 <212> TYPE: PRT
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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139      1              5
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159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
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166 Ala Glu Lys Leu Ser Gly Thr
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189 <220> FEATURE:
190 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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195      1              5              10              15
197 Arg Ser Pro Arg
198      20
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202 <211> LENGTH: 21
203 <212> TYPE: PRT

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204 &lt;213&gt; ORGANISM: Artificial Sequence

206 &lt;220&gt; FEATURE:

207 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

210 &lt;400&gt; SEQUENCE: 14

211 Lys Leu Ser Lys Gln Gly Arg Pro Leu Asn Asp Met Lys Gln Glu Leu

212 1 5 10 15

214 Thr Thr Glu Phe Arg

215 20

218 &lt;210&gt; SEQ ID NO: 15

219 &lt;211&gt; LENGTH: 1201

220 &lt;212&gt; TYPE: DNA

221 &lt;213&gt; ORGANISM: Homo sapiens

223 &lt;400&gt; SEQUENCE: 15

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225 agtgaaactt tgtatataat gaatagaata ataaaagatt atgttggatg actagtctgt 120
226 aattgcctca aggaaagcat acaatgaata agttattttg gtacttcctc aaaatagcca 180
227 acacaatagg gaaatggaga aaatgtactc tgaacaccat gaaaaggga cctgaaaatc 240
228 taatgtgtaa acttgagaa atgacattag aaaacgaaag ctacaaaaga gaacactctt 300
229 caaaataatc tgagatgcat gaaaggcaaa cattcactag agctggaatt tccctaagtc 360
230 tatgcaggga taagtagcat atttgacctt caccatgatt atcaagcact tctttggaac 420
231 tgtgttggtg ctgctggcct ctaccactat cttctctcta gatttgaaac tgattatctt 480
232 ccagcaaaga caagtgaatc aagaaagttt aaaactcttg aataagttgc aaacctgttc 540
233 aattcagcag tgtctaccac acaggaaaaa ctttctgctt cctcagaagt ctttgagtcc 600
234 tcagcagtac caaaaaggac acactctggc cattctccat gagatgcttc agcagatctt 660
235 cagcctcttc agggcaaata tttctctgga tgggtgggag gaaaaccaca cggagaaatt 720
236 cctcattcaa cttcatcaac agctagaata cctagaagca ctcatgggac tggaagcaga 780
237 gaagctaagt ggtactttgg gtatgataa ccttagatta caagttaaaa tgtacttccg 840
238 aaggatccat gattacctgg aaaaccagga ctacagcacc tgtgcctggg ccattgtcca 900
239 agtagaaatc agccgatgtc tgttctttgt gttcagtcct acagaaaaac tgagcaaaca 960
240 aggaagaccc ttgaacgaca tgaagcaaga gcttactaca gagtttagaa gcccgaggta 1020
241 ggtggaggga ctagaggact tctccagaca tgattcttca tagagtggta atacaattta 1080
242 tagtacaatc acattgcttt gattttgtgt atatatatat ttatctgtgt tttaagattg 1140
243 tgcattattga ccacaattgt ttttattttg taatgtggct ttatatattc tatccatttt 1200
244 a

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247 &lt;210&gt; SEQ ID NO: 16

248 &lt;211&gt; LENGTH: 208

249 &lt;212&gt; TYPE: PRT

250 &lt;213&gt; ORGANISM: Homo sapiens

252 &lt;400&gt; SEQUENCE: 16

253 Met Ile Ile Lys His Phe Phe Gly Thr Val Leu Val Leu Leu Ala Ser

254 1 5 10 15

256 Thr Thr Ile Phe Ser Leu Asp Leu Lys Leu Ile Ile Phe Gln Gln Arg

257 20 25 30

259 Gln Val Asn Gln Glu Ser Leu Lys Leu Leu Asn Lys Leu Gln Thr Leu

260 35 40 45

262 Ser Ile Gln Gln Cys Leu Pro His Arg Lys Asn Phe Leu Leu Pro Gln

263 50 55 60

265 Lys Ser Leu Ser Pro Gln Gln Tyr Gln Lys Gly His Thr Leu Ala Ile

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266 65          70          75          80
268 Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe Arg Ala Asn Ile
269          85          90          95
271 Ser Leu Asp Gly Trp Glu Glu Asn His Thr Glu Lys Phe Leu Ile Gln
272          100          105          110
274 Leu His Gln Gln Leu Glu Tyr Leu Glu Ala Leu Met Gly Leu Glu Ala
275          115          120          125
277 Glu Lys Leu Ser Gly Thr Leu Gly Ser Asp Asn Leu Arg Leu Gln Val
278          130          135          140
280 Lys Met Tyr Phe Arg Arg Ile His Asp Tyr Leu Glu Asn Gln Asp Tyr
281 145          150          155          160
283 Ser Thr Cys Ala Trp Ala Ile Val Gln Val Glu Ile Ser Arg Cys Leu
284          165          170          175
286 Phe Phe Val Phe Ser Leu Thr Glu Lys Leu Ser Lys Gln Gly Arg Pro
287          180          185          190
289 Leu Asn Asp Met Lys Gln Glu Leu Thr Thr Glu Phe Arg Ser Pro Arg
290          195          200          205
293 <210> SEQ ID NO: 17
294 <211> LENGTH: 187
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296 <213> ORGANISM: Unknown Organism
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Description of Unknown Organism: IFNB amino
300 acid sequence
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304 1          5          10          15
306 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
307          20          25          30
309 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
310          35          40          45
312 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
313          50          55          60
315 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
316 65          70          75          80
318 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
319          85          90          95
321 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
322          100          105          110
324 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
325          115          120          125
327 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
328          130          135          140
330 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
331 145          150          155          160
333 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
334          165          170          175
336 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
337          180          185

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**VERIFICATION SUMMARY**

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